

Erratum

New Phytologist **167** (2005), 129–142

Since its publication, the authors of Gupta *et al.* (2005) have brought to our attention corrections that need to be made to Table 2 in their paper. The corrected table is printed below.

We apologize to our readers for this mistake.

Reference

Gupta P, Duplessis S, White H, Karnosky DF, Martin F, Podila GK. 2005. Gene expression patterns of trembling aspen trees following long-term exposure to interacting elevated CO₂ and troposphere O₃. *New Phytologist* **165**: 129–142.

Table 2 Regulation of gene expression for selected significantly regulated genes in leaves of aspen (*Populus tremuloides*) grown under elevated CO₂, elevated O₃ and combined elevated CO₂ and O₃ concentrations compared with control conditions (C)

Clone ID	Accession no.	Gene function	CO ₂ /C	In <i>P</i> -value	O ₃ /C	In <i>P</i> -value	O ₃ + CO ₂ /C	In <i>P</i> -value	SOM cluster	RNA blot
F02G09	CA820757	Hypothetical protein	1.76	0.01229	1.59		1.46	0.03878	c12	
R18B06	CA822984	Cysteine protease	1.37	0.01332	1.88	0.04904	1.79	0.03431	c12	*
R75F07	CA826280	ACC oxidase	-1.22	0.00952	1.27	0.02943	1.86		c11	*
RA01F02	CA821251	Ribulose-5-phosphate-3-epimerase	-1.43	0.04338	1.07		-1.08		c4	
R74G09	CA826232	Aquaporin	-1.58	0.0238	1.07		1.02		c8	
R10A04	CA822570	Wound-induced protein	1.38		2.57	0.0338	1.89		c13	*
R04C10	CA822148	Calmodulin 1	1.29		1.94	0.04808	1.62	0.00365	c12	
R12E11	CA822712	Sucrose synthase	1.22		1.91	0.04547	1.62		c12	
R27H05	CA823548	Ubiquitin/ribosomal protein S27a	1.14		1.87	0.02579	1.74		c12	
R08B12	CA822430	Zinc-finger protein	1.27		1.86	0.00712	1.62	0.02152	c12	
R33H02	CA823880	Histone H4	1.56		1.84	0.026	2.07		c13	
R06C05	CA822298	Histone H3	1.41		1.84	0.00295	1.95		c13	
R22D07	CA823207	Ribosomal protein L8	1.17		1.82	0.00762	1.56	0.0069	c9	
R25F07	CA823402	Inorganic pyrophosphatase	1.21		1.81	0.02828	1.39	0.04062	c9	
R21B12	CA823125	ATP-citrate lyase	1.37		1.81	0.0033	1.66	0.03525	c12	
F11C02	CA821163	60S acidic ribosomal protein L12	1.09		1.8	0.03842	1.43	0.01225	c9	
R10G01	CA822614	Kinetochore-associated protein Skp1	-1.03		1.8	0.01635	1.36	0.0438	c8	
R03D06	CA822075	Alcohol dehydrogenase	-1.01		1.78	0.02634	1.31		c8	
R02H08	CA822034	Glutamine synthetase	-1.07		1.69	0.04107	1.4		c8	
F11A19	CA821143	Rubisco small subunit	-1.27		-1.98	0.00052	-1.47	0.03338	c0	*
R71C08	CA826021	Aquaporin	-1.18		1.55		2.46	0.0153	c11	
R77F06	CA826403	Formate dehydrogenase	-1.12		1.99		2.36	0.04624	c11	
R75C04	CA826255	G3PDH	-1.17	0.02355	1.49	0.01327	2.34	0.00628	c11	
R46C01	CA824657	Pop3 wound-induced protein	1.07		1.68	0.0078	2.22	0.0003	c13	*
R57F07	CA825362	Naringenin-chalcone synthase	1.02		1.47		2.11	0.04185	c13	
R57C09	CA825341	Mitochondrial phosphate transporter	-1.31		1.43		2.05	0.04031	c11	
R73E09	CA826154	Dehydrin	-1.04		1.45		1.97	0.0112	c11	
R20E04	CA823085	Beta tubulin 1	1.3		1.65	0.04973	1.91	0.02682	c13	
R20A02	CA823050	Elongation factor eF-2	1.07		1.48		1.91	0.04272	c10	
F11B12	CA821155	Thaumatococcus-like protein	1.63		1.63		1.87	0.03375	c12	
R17C05	CA822967	Hypothetical protein	-1.02		1.72	0.02518	1.77	0.01793	c11	
R25G01	CA823406	S-adenosylmethionine synthetase	1.2		1.35		1.77	0.03061	c10	*
R16G02	CA822945	Alpha-6 tubulin	1.33		1.63	0.01647	1.75	0.03363	c12	
R16G03	CA822946	Xyloglucan endotransglycosylase	1.78		1.44	0.01327	1.75	0.0078	c12	
R77F05	CA826402	Polyubiquitin	1.49		1.99		1.71	0.04684	c12	
F11B16	CA821159	Carbonate dehydratase	1.02		-1.37		-1.82	0.03151	c1	
F02E05	CA820743	Rubisco small subunit	-1.34		-1.78	0.00123	-1.88	0.04585	c0	*

Associated In *P*-values < 0.05 as calculated by the Cyber-T program between year-replicates 2001 and 2002 are given along with mean ratios. These genes were selected from Table S1 for their high level of regulation of expression. Rows are sorted by level of regulation measured in the three different treatments. Signal ratios < 1.0 were inverted and multiplied by -1 to aid their interpretation. Mean ratios highlighted in gray indicate genes that showed similar expression patterns in years 2001 and 2002. The self-organizing map (SOM) cluster column indicates the corresponding cluster in Fig. 2. The asterisk indicates genes tested by RNA blots. ACC oxidase, 1-aminocyclopropane-1-carboxylate oxidase.